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## *Annotating Arabidopsis*

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Jonathan B Weitzman

Email: jonathanweitzman@hotmail.com

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Now that the *Arabidopsis thaliana* genome has been sequenced, plant biologists are turning their efforts to genome annotation. In a report published on the *Scienceexpress* website, Motoaki Seki and colleagues from the *RIKEN Institute* in Japan, describe a large-scale analysis of full-length *Arabidopsis* cDNA libraries (*Scienceexpress*, 21 March 2002 10.1126/science.1071006). They isolated over 150,000 *RIKENArabidopsisFull-Length (RAFL) cDNA clones*, sequenced the ends and clustered them into almost 15,000 non-redundant groups. To generate the clones they constructed 19 cDNA libraries from plants grown under various conditions of stress, hormone and light. To optimize library construction they used the *biotinylated CAP trapper method*, using trehalose-thermoactivated reverse transcriptase combined with a single-strand linker ligation step, and normalization and subtraction procedures. They also created a database of promoter sequences upstream of RAFL clones. Amongst the clones were 837 that had been missed by previous annotation efforts; this project therefore makes a significant contribution to attempts to annotate the *Arabidopsis* genome. The current tally of experimentally confirmed *Arabidopsis* genes is 17,956.

## References

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4. Plant functional genomics research group, [<http://www.gsc.riken.go.jp/Plant/index.html>]
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